AMENDMENTS TO THE SPECIFICATION

This Amendment to the specification will replace all prior versions, for the sections indicated:

Please replace the paragraph on page 3, lines 23-27 with the following:

The invention also ~~regards~~ is directed to a polypeptide as described above of up to about 427 amino acids in length possessing a phosphodiesterase 7 catalytic domain and comprising at least 312 consecutive amino acids of a sequence selected from the group consisting of the amino acid sequences of SEQ ID ~~№~~ NOs:1, 2 ~~or~~ and 3; or a homologous polypeptide thereof.

Please replace the paragraph on page 3, line 29 through page 4, line 12 with the following:

Said polypeptide comprises the ~~aminoacid~~ amino acid sequence which:

- begins at the ~~aminoacid~~ amino acid residue located in position 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 ,11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64 of SEQ ID ~~№~~NOs:1, 2 or 3; and which
- ends at the ~~aminoacid~~ amino acid residue located in position 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 934, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427 of SEQ ID ~~№~~ NOs:1, 2 or 3; or a homologous peptide thereof.

Please replace the paragraph on page 4, lines 14-22 with the following:

The polypeptides comprising the amino acid sequence beginning at the amino acid residue in position 5 and ending at the amino acid residue in position 427 of SEQ ID ~~№~~ NOs:1, 2 or 3; and/or those beginning at the amino acid residue in position 25 and ending at the amino acid residue in position 427 of

SEQ ID ~~Nº~~ NOs:1, 2 or 3; and/or those beginning at the amino acid residue in position 45 and ending at the amino acid residue in position 394 of SEQ ID ~~Nº~~ NOs:1, 2 or 3; and/or those beginning at the amino acid residue in position 45 and ending at the amino acid residue in position 427 of SEQ ID ~~Nº~~ NOs:1, 2 or 3 are preferred.

Please replace the paragraph on page 4, lines 24-29 with the following:

The polypeptides comprising the amino acid sequence beginning at the amino acid residue in position 45 and ending at the amino acid residue in position 394 of SEQ ID ~~Nº~~ NOs:1, 2 or 3; and the polypeptide comprising the amino acid sequence beginning at the amino acid residue in position 45 and ending at the amino acid residue in position 427 of SEQ ID ~~Nº~~ NOs:1, 2 or 3 are most preferred.

Please replace the paragraph on page 5, lines 14-16 with the following:

A further aspect of this invention is a nucleic acid sequence which is selected from the group consisting of the nucleic acid sequences of SEQ ID ~~Nº~~ NOs:4, 5 ~~or~~ and 6; or a sequence complementary thereto.

Please replace the paragraph on page 7, lines 16-19 with the following:

Said method wherein the polypeptide provided at step a) consists of the amino acid sequence beginning at the amino acid residue in position 45 and ending at the amino acid residue in position 427 of SEQ ID ~~Nº~~ NO:1, or a homologous polypeptide thereof.

Please replace the paragraph on page 12, lines 11-16 with the following:

2) A polypeptide according to 1) above of up to about 427 amino acids in length possessing a phosphodiesterase 7 catalytic domain and comprising at least 312 consecutive amino acids of a sequence selected from the group consisting of the amino acid sequences of SEQ ID ~~Nº~~ NOs:1, 2 ~~or~~ and 3; or a homologous polypeptide thereof.

Please replace the paragraph on page 12, line 18 through page 13, line 2 with the following:

3) The polypeptide according to 2) above which comprises the ~~aminoacid~~ amino acid sequence which:

- begins at the ~~aminoacid~~ amino acid residue located in position 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 ,11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64 of SEQ ID ~~N°~~NOs:1, 2 or 3; and which

- ends at the ~~aminoacid~~ amino acid residue located in position 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 934, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427 of SEQ ID ~~NOs:~~1, 2 or 3; or a homologous peptide thereof.

Please replace the paragraph on page 13, lines 4-7 with the following:

4) The polypeptide according to 3) above which comprises the amino acid sequence beginning at the amino acid residue in position 5 and ending at the amino acid residue in position 427 of SEQ ID ~~N°~~ NOs:1, 2 or 3; or a homologous polypeptide thereof.

Please replace the paragraph on page 13, lines 9-12 with the following:

5) The polypeptide according to 3) above which comprises the amino acid sequence beginning at the amino acid residue in position 25 and ending at the amino acid residue in position 427 of SEQ ID ~~N°~~ NOs:1, 2 or 3; or a homologous polypeptide thereof.

Please replace the paragraph on page 13, lines 14-17 with the following:

6) The polypeptide according to 3) above which comprises the amino acid sequence beginning at the amino acid residue in position 45 and ending at the

amino acid residue in position 427 of SEQ ID ~~Nº~~ NOs:1, 2 or 3; or a homologous polypeptide thereof.

Please replace the paragraph on page 13, lines 19-22 with the following:

7) The polypeptide according to 3) above which comprises the amino acid sequence beginning at the amino acid residue in position 5 and ending at the amino acid residue in position 394 of SEQ ID ~~Nº~~ NOs:1, 2 or 3; or a homologous polypeptide thereof.

Please replace the paragraph on page 13, lines 24-27 with the following:

8) The polypeptide according to 3) above which comprises the amino acid sequence beginning at the amino acid residue in position 25 and ending at the amino acid residue in position 394 of SEQ ID ~~Nº~~ NOs:1, 2 or 3; or a homologous polypeptide thereof.

Please replace the paragraph on page 13, lines 29-32 with the following:

9) The polypeptide according to 3) above which comprises the amino acid sequence beginning at the amino acid residue in position 45 and ending at the amino acid residue in position 394 of SEQ ID ~~Nº~~ NOs:1, 2 or 3; or a homologous polypeptide thereof.

Please replace the paragraph on page 14, lines 24-26 with the following:

15) The nucleic acid sequence according to 14) above which is selected from the group consisting of the nucleic acid sequences of SEQ ID ~~Nº~~ NOs:4, 5 ~~or~~ and 6; or a sequence complementary thereto.

Please replace the paragraph on page 23, lines 3-8 with the following:

Figure 1 illustrates the alignment between the ~~aminoacid~~ amino acid sequences of two of the human PDE7 isoforms, respectively PDE7A1 (labelled h7A1.PRO) and PDE7A2 (labelled h7A2.PRO) as well as the mouse PDE7A2 (labelled mou7A2.PRO) and the rat PDE7A1 (labelled rat7.a.PRO) proteins.

~~Aminoacid~~ Amino acid residues which aren't boxed denote ~~aminoacid~~ amino acids which are not homologous for the four ~~aminoacids~~ amino acid sequences.

Please replace the paragraph on page 27, lines 26-31 with the following:

The primary ~~aminoacid~~ amino acid sequence of PDE7A is most closely related to the PDE4 family of PDEs, despite a relatively weak ~~aminoacid~~ amino acid identity. Indeed, the ~~aminoacid~~ amino acid sequence identity between PDE7A and PDE4 is of about 25% on the overall sequence. However, the ~~aminoacid~~ amino acid sequence identity between PDE7 and PDE4 reaches about 35% within the most conserved regions.

Please replace the paragraph on page 35, lines 23-32, through page 36, lines 1-4, with the following:

Through ~~aminoacid~~ amino acid deletion experiments presented in the examples below, the inventors have shown that a polypeptide consisting of the sequence beginning at position 61 or 81 and ending at position 483 of the human PDE7A1 ~~aminoacid~~ amino acid sequence possesses a phosphodiesterase catalytic activity increased respectively by eight or nine fold as compared with the phosphodiesterase catalytic activity of the endogenous PDE7A1 or PDE7A2 full length proteins. Moreover, the inventors have also shown that a further increased phosphodiesterase catalytic activity could be observed for shorter polypeptides. For example, a polypeptide consisting of an ~~aminoacid~~ amino acid sequence starting at position 101 and ending at position 450 of the ~~aminoacid~~ amino acid sequence of human PDE7A1 exhibited a phosphodiesterase catalytic activity about 15 fold higher than the catalytic activity of the endogenous PDE7A1 and PDE7A2 full length proteins.

Please replace the paragraphs on page 36, lines 11-32, through page 37, lines 1-22, with the following:

Consequently, a first object of the present invention is a polypeptide of up to about 427 ~~aminoacids~~ amino acids in length possessing a phosphodiesterase 7 catalytic domain and comprising at least 312 consecutive ~~aminoacids~~ amino acids of the sequence of SEQ ID ~~№~~ NO:1, or a homologous polypeptide thereof.

An ~~aminoacid~~ amino acid sequence alignment between the human PDE7A1 and PDE7A2 ~~aminoacid~~ amino acid sequences and the PDE7 ~~aminoacid~~ amino acid sequences originating, respectively, from mouse and rat, has shown a high ~~aminoacid~~ amino acid identity between the human and the mouse or the rat sequences. More precisely, between the ~~aminoacid~~ amino acid at position 57 and the ~~aminoacid~~ amino acid in position 483 of the human PDE7A1 protein, a 93.7% ~~aminoacid~~ amino acid identity with the corresponding mouse PDE7A2 ~~aminoacid~~ amino acid sequence and a 94.1 % ~~aminoacid~~ amino acid identity with the rat PDE7A1 ~~aminoacid~~ amino acid sequence is observed.

Therefore, the ~~aminoacid~~ amino acid sequences, derived, respectively, from the PDE7A mouse and rat ~~aminoacid~~ amino acid sequences, and which, share a high ~~aminoacid~~ amino acid identity with the human sequence of SEQ ID ~~N°~~ NO:1 also comprise the catalytic domain of the mouse or the rat PDE7 enzymes.

The mouse ~~aminoacid~~ amino acid sequence derived from the mouse PDE7A2 sequence, and which aligns with the human sequence of SEQ ID ~~N°~~ NO:1, is referred to as the ~~aminoacid~~ amino acid sequence of SEQ ID ~~N°~~ NO:2.

The rat ~~aminoacid~~ amino acid sequence derived from the rat PDE7A1 sequence, and which aligns with the human ~~aminoacid~~ amino acid sequence of SEQ ID ~~N°~~ NO:1, is referred to as the ~~aminoacid~~ amino acid sequence of SEQ ID ~~N°~~ NO:3.

A further object of the present invention consists of a polypeptide of up to about 427 ~~aminoacids~~ amino acids in length possessing a phosphodiesterase 7 catalytic domain and comprising at least 312 consecutive ~~aminoacids~~ amino acids of a sequence selected from the group consisting of the ~~aminoacid~~ amino acid sequences of SEQ ID ~~N°~~ NOs:2 and 3; or a homologous polypeptide thereof.

For the purpose of the present invention, a " homologous polypeptide " encompasses polypeptides having at least 80%, more preferably at least 85%, most preferably 90 or 95% identity in ~~aminoacids~~ amino acids as regards the ~~aminoacid~~ amino acid sequences of SEQ ID ~~N°~~ NOs:1, 2 and 3 above. The

changes in ~~aminoacid~~ amino acid residues of a homologous polypeptide of the invention consist of ~~aminoacid~~ amino acid changes ranging from 1, 2, 3, 4, 5, 10 to 20 substitutions, additions or deletions of one ~~aminoacid~~ amino acid as regards the reference polypeptide.

In all cases, the " homologous polypeptide " exhibits a PDE7 phosphodiesterase catalytic activity which is at least of the same order of magnitude as the phosphodiesterase catalytic activity measured for the polypeptide having the ~~aminoacid~~ amino acid sequence of SEQ ID ~~N°~~ NO:1. In other words, a " homologous polypeptide " according to the invention possesses a phosphodiesterase activity of preferably at least six fold, and most preferably at least eight fold, the catalytic activity which is observed with the endogenous full length human PDE7A1 or PDE7A2 proteins.

Please replace the paragraphs on page 38, lines 3-31, through page 39, lines 1-11, with the following:

Another object of the invention is a polypeptide as defined above which comprises an ~~aminoacid~~ amino acid sequence which:.

- begins at the ~~aminoacid~~ amino acid residue located in position 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 ,11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64 of SEQ ID N°1, 2 or 3; and which

- ends at the ~~aminoacid~~ amino acid residue located in position 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 934, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427 of SEQ ID N°1, 2 or 3; or a homologous peptide thereof.

Preferred polypeptides according to the invention are:

A polypeptide which comprises the ~~aminoacid~~ amino acid sequence beginning in position 5 and ending in position 427 of SEQ ID ~~N°~~ NOs:1, 2 or 3; or a homologous polypeptide thereof.

A polypeptide which comprises the ~~aminoacid~~ amino acid sequence beginning in position 25 and ending in position 427 of SEQ ID ~~N°~~ NOs:1, 2, or 3; or a homologous polypeptide thereof.

A polypeptide which comprises the ~~aminoacid~~ amino acid sequence beginning in position 45 and ending in position 427 of SEQ ID ~~N°~~ NOs:1, 2 or 3; or a homologous polypeptide thereof.

A polypeptide which comprises the ~~aminoacid~~ amino acid sequence beginning in position 45 and ending in position 394 of SEQ ID ~~N°~~ NOs:1, 2 or 3; or a homologous polypeptide thereof.

Most preferred polypeptides according to the invention are:

A polypeptide which comprises the ~~aminoacid~~ amino acid sequence beginning in position 45 and ending in position 427 of SEQ ID ~~N°~~ NOs:1, 2 or 3; or a homologous polypeptide thereof.

A polypeptide which comprises the ~~aminoacid~~ amino acid sequence beginning in position 45 and ending in position 394 of SEQ ID ~~N°~~ NOs:1, 2 or 3; or a homologous polypeptide thereof.

It has been shown according to the invention that the polypeptides 45-427 and 45-394 described above which are derived from the ~~aminoacid~~ amino acid sequence of SEQ ID ~~N°~~ NO:1, exhibit about 15 times more phosphodiesterase catalytic activity than the endogenous full length PDE7A1 and PDE7A2 proteins.

Please replace the paragraphs on page 39, lines 16-30, through page 40, lines 1-31, with the following:

A further object of the invention is a nucleic acid sequence which encodes a polypeptide of up to about 427 ~~aminoacids~~ amino acids in length possessing a phosphodiesterase 7 catalytic domain and comprising at least 312 consecutive ~~aminoacids~~ amino acids of a sequence selected from the group consisting of the

amino acid sequences of SEQ ID ~~Nº~~ NO:1, 2 ~~or~~ and 3; or a homologous polypeptide thereof.

The following preferred nucleic acids are encompassed by the present invention:

- a nucleic acid encoding an ~~polypeptide~~ amino acid sequence as defined above which comprises the ~~aminoacid~~ amino acid sequence which:

- begins at the ~~aminoacid~~ amino acid residue located in position 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 ,11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64 of SEQ ID ~~Nº~~ NOs:1, 2 or 3; and which

- ends at the ~~aminoacid~~ amino acid residue located in position 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 934, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427 of SEQ ID ~~N~~ NOs:1, 2 or 3; or a homologous peptide thereof.

- a nucleic acid encoding an ~~polypeptide~~ amino acid sequence which begins at the ~~aminoacid~~ amino acid residue in position 5 and ends at the ~~aminoacid~~ amino acid residue in position 427 of SEQ ID ~~Nº~~ NOs:1, 2 or 3; or a homologous polypeptide thereof, and a nucleic acid sequence complementary thereto;

- a nucleic acid encoding an ~~polypeptide~~ amino acid sequence which begins at the ~~aminoacid~~ amino acid residue in position 25 and ends at the ~~aminoacid~~ amino acid residue in position 427 of SEQ ID ~~Nº~~ NOs:1, 2 or 3; or a homologous polypeptide thereof, and a nucleic acid sequence complementary thereto;

- a nucleic acid encoding an ~~polypeptide~~ amino acid sequence which begins at the ~~aminoacid~~ amino acid residue in position 45 and ends at the ~~aminoacid~~ amino acid residue in position 427 of SEQ ID ~~Nº~~ NOs:1, 2 or 3; or a

homologous polypeptide thereof, and a nucleic acid sequence complementary thereto;

- a nucleic acid encoding an ~~polypeptide~~ amino acid sequence which begins at the ~~aminoacid~~ amino acid residue in position 45 and ends at the ~~aminoacid~~ amino acid residue in position 394 of SEQ ID ~~Nº~~ NOs:1, 2 or 3; or a homologous polypeptide thereof, and a nucleic acid sequence complementary thereto.

In a first preferred embodiment, the nucleic acid sequence is that of SEQ ID ~~Nº~~NO:4, which encodes the human ~~polypeptide~~ amino acid sequence of SEQ ID ~~Nº~~ NO:1, or a nucleic acid sequence complementary thereto.

In a second preferred embodiment, the nucleic acid sequence is that of SEQ ID ~~Nº~~ NO:5, which encodes the mouse ~~polypeptide~~ amino acid sequence of SEQ ID ~~Nº~~ NO:2, or a nucleic acid sequence complementary thereto.

In a third preferred embodiment, the nucleic acid sequence is that of SEQ ID ~~Nº~~ NO:6, which encodes the rat ~~polypeptide~~ amino acid sequence of SEQ ID ~~Nº~~ NO:3, or a nucleic acid sequence complementary thereto.

Please replace the paragraph on page 50, lines 8-13 with the following:

Thus, in a first embodiment, a recombinant host cell according to the invention comprises a nucleic acid encoding a polypeptide of up to about 427 ~~aminoacids~~ amino acids in length possessing a phosphodiesterase 7 catalytic domain and comprising at least 312 consecutive ~~aminoacids~~ amino acids of a sequence selected from the group consisting of the aminoacid sequences of SEQ ID ~~Nº~~ NO:1, 2 ~~or~~ and 3; or a homologous polypeptide thereof.

Please replace the paragraphs on page 50, lines 26-31 with the following:

a) prokaryotic host cells : *Escherichia coli* strains, *Bacillus subtilis*, or *Salmonella typhimurium*, Sf9 cells (ATCC ~~Nº~~NO. CRL 1711), Sf21 cells (Cawley P. et al. 1977);

b) eukaryotic host cells: HeLa cells (ATCC ~~№~~ NO. CRL2), COS cells (ATCC ~~№~~NO. CRL 1650; ~~№~~ NO. CRL 1651) or CHO cells (ATCC ~~№~~ NO. CCL-61).

Please replace the paragraph on page 51, lines 20-30 with the following:

Preferred ES cell lines according to the invention are the following: ES-E14 TG2a (ATCC ~~№~~ NO. CRL-1821) ES-D3 (ATCC ~~№~~ NO. CRL 1934 and ~~№~~NO. CRL-11632), TS001 (ATCC ~~№~~ NO. CRL-11776), and 36.5 (ATCC ~~№~~ NO. CRL-11116). To maintain ES cells in an uncommitted state, they are cultured in the presence of growth inhibited feeder cells which provide the appropriate signals to preserve this embryonic phenotype and serve as a matrix for ES cell adherence. Preferred feeder cells consist of primary embryonic fibroblasts that are established from tissue of day 13-day 14 embryos of virtually any mouse strain, that are maintained in culture, such as described by ABBONDANZO et al. (1993), or by the presence of an inhibitory concentration of LIF, such as described by PEASE and WILLIAMS (1990).

Please replace the paragraph on page 52, lines 20-24 with the following:

In a preferred embodiment of the first method of screening described above the polypeptide added at step a) consists of the amino acid sequence beginning at the amino acid residue in position 45 and ending at the amino acid residue in position 427 of SEQ ID ~~№~~ NO:1, or a homologous polypeptide thereof.

Please replace the paragraph on page 62, lines 29-31 with the following:

PDE7A1 CGGGGATCCATGGAAGTGTGTTACCAG (SEQ ID ~~№~~ NO:12)
PDE7A2 CGCGTCTAGATTATGATAACCGATTTTCCTGAGGTAA (SEQ ID ~~№~~ NO:13)

Please replace the paragraph on page 63, lines 16-19 with the following:

PDE7AK1 CGGGATCCGCCACCATGGAAGTGTGTTACC (SEQ ID ~~№~~ NO:14)

PDE7AK2 CGCGTCTAGATTATGATAACCGATTTTCCTGAGGTAA (SEQ ID ~~№~~ NO:13)

Please replace the paragraphs on page 63, lines 25-31 with the following:

UCR3'1 CCGGGGGTACCGGCGGCCGCGGCAGGGCGGGCGCCG (SEQ ID ~~№~~ NO:15)

UCR3'2 GGGGGATCCTGAATACGCCCGCCCTGCCTCCG (SEQ ID ~~№~~ NO:16)

UCR5'1 GGGTCTAGACCCCAGAACCAGTGGGACAAACTGCCTCCT (SEQ ID ~~№~~ NO:17)

UCR5'2 GGCGGGCCCTGGAGAAACATAACATGCACGTCAC SEQ ID ~~№~~ NO:18)

Please replace the paragraph on page 64, lines 25-27 with the following:

H1 CCGGGATCCGACAGGCCGGTCCCCCAGCACGTCCTC (SEQ ID ~~№~~ NO:19)

H2 CGCGTCTAGATTATGATAACCGATTTTCCTGAGG (SEQ ID ~~№~~ NO:20)

Please replace the paragraphs on page 65, lines 1-28 with the following:

A1 CCGGGATCCCCCCGGCAGCTCTCTCAGAGGCGT (SEQ ID ~~№~~ NO:21)

H2 CGCGTCTAGATTATGATAACCGATTTTCCTGAGG (SEQ ID ~~№~~ NO:20)

The following primers were used to make the construct PDE7Δ60 which lacks the first 60 amino acids to generate PDE7A;61 – 483.

B1 CCGGGATCCTTATACATTCGTATGCTAGGAG (SEQ ID ~~№~~ NO:22)

H2 CGCGTCTAGATTATGATAACCGATTTTCCTGAGG (SEQ ID ~~№~~ NO:20)

The following primers were used to make the construct PDE7Δ80 which lacks the first 80 amino acids to generate PDE7A;81 – 483.

C1 CCGGGATCCAGAAGAGGTTCTCACCCATATA (SEQ ID ~~№~~ NO:23)

H2 CGCGTCTAGATTATGATAACCGATTTTCCTGAGG (SEQ ID ~~№~~ NO:20)

The following primers were used to make the construct PDE7Δ100 which lacks the first 100 amino acids to generate PDE7A;101 – 483.

D1 CCGGGGATCCGTGTCTGTCTCTGCAAGGAATATCAGA (SEQ ID ~~№~~ NO:24)

H2 CGCGTCTAGATTATGATAACCGATTTTCCTGAGG (SEQ ID ~~№~~ NO:20)

Please replace the paragraph on page 66, lines 4-5 with the following:

F1 CCGGGGATCCAATGGACAAGCCAAGTGTATGCT (SEQ ID ~~№~~ NO:26)

H2 CGCGTCTAGATTATGATAACCGATTTTCCTGAGG (SEQ ID ~~№~~ NO:20)

Please replace the paragraphs on page 66, lines 18-27 with the following:

The construct PDE7:101- 450 was made using the following primers.

D1 CCGGGGATCCGTGTCTGTCTCTGCAAGGAATATCAGA (SEQ ID ~~№~~ NO:24)

I2 CGCGTCTAGATTAGCTGGCTTTATTCAGCC (SEQ ID ~~№~~ NO:28)

The construct PDE7:101 - 430 was made using the following primers.

D1 CCGGGGATCCGTGTCTGTCTCTGCAAGGAATATCAGA (SEQ ID ~~№~~ NO:24)

J2 CGCGTCTAGATTACCTGGCCCATTCTGTAAATAAA (SEQ ID ~~№~~ NO:29)

Please replace the paragraph on page 67, lines 1-4 with the following:

D1 CCGGGGATCCGTGTCTGTCTCTGCAAGGAATATCAGA (SEQ ID ~~№~~ NO:24)

K2 CGCGTCTAGATTATAGGTAAGTCATAAAACCAATCT (SEQ ID ~~№~~ NO:30)